## STIC Biotechnology Systems Branch

## RAW SEQUENCE LISTING
##    ERROR REPORT

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Application Serial Number: _/0/5/7,/55_
Source: _PCT_
Date Processed by STIC: _3/31/06_

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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Any reply·including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06

**PCT**

**RAW SEQUENCE LISTING**
**PATENT APPLICATION:  US/10/517,155**

DATE: 03/31/2006
TIME: 15:12:17

Input Set : **A:\211080011U6.TXT**
Output Set: **N:\CRF4\03312006\J517155.raw**

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 4 <110> APPLICANT: Chang, Chawnshang
 6 <120> TITLE OF INVENTION: Androgen Receptor Coregulators
 9 <130> FILE REFERENCE: 21108.0011U6
11 <140> CURRENT APPLICATION NUMBER: 10/517,155
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C--> `12 <141> CURRENT FILING DATE: 2004-12-06`

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14 <150> PRIOR APPLICATION NUMBER: PCT/US03/17937
15 <151> PRIOR FILING DATE: 2003-06-06
17 <150> PRIOR APPLICATION NUMBER: US 60/387,087
18 <151> PRIOR FILING DATE: 2002-06-06
20 <160> NUMBER OF SEQ ID NOS: 47
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1721
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapien
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (40)...(1464)
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (1120)...(1452)
36 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the
37       C-terminal domain
39 <220> FEATURE:
40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (697)...(834)
42 <223> OTHER INFORMATION: Coding sequence and polypeptide region which may
43       form a cystein-rich RING finger motif
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: (964)...(1089)
48 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
49       cystein-rich B box like structure
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52 ggtctctggt ctcccctctc tgagcactct gaggtcctt atg tcg tca gaa gat        54
53                                                Met Ser Ser Glu Asp
54                                                 1               5
56 cga gaa gct cag gag gat gaa ttg ctg gcc ctg gca agt att tac gat      102
57 Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp
58              10                  15                  20
60 gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg      150
61 Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg
62              25                  30                  35
```

*pp 6-7*

*Does Not Comply*
*Corrected Diskette Needed*

```
64 atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat      198
65 Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn
66          40                  45                  50
68 tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt      246
69 Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe
70          55                  60                  65
72 ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc      294
73 Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser
74 70                  75                  80                  85
76 tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act      342
77 Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr
78                  90                  95                  100
80 cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac      390
81 Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His
82                  105                 110                 115
84 cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag      438
85 Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu
86          120                 125                 130
88 acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt      486
89 Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly
90          135                 140                 145
92 tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca      534
93 Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr
94 150                 155                 160                 165
96 gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa      582
97 Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu
98                  170                 175                 180
100 att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg     630
101 Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu
102          185                 190                 195
104 atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt     678
105 Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe
106          200                 205                 210
108 aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt     726
109 Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly
110          215                 220                 225
112 agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc     774
113 Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala
114 230                 235                 240                 245
116 tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa     822
117 Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln
118                  250                 255                 260
120 tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt     870
121 Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly
122                  265                 270                 275
124 cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc     918
125 Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg
126          280                 285                 290
128 ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc     966
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```
129 Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys
130     295                 300                 305
132 ccc cgg ccg tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc    1014
133 Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr
134 310                 315                 320                 325
136 atg ggt atc tgc tcc agc tgc aat ttt gcc ttc tgt act ttg tgc agg    1062
137 Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg
138                 330                 335                 340
140 ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta    1110
141 Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val Thr Ala Glu Lys Leu
142                 345                 350                 355
144 atg gac tta cga aat gaa tac ctg caa gcg gat gag gct aat aaa aga    1158
145 Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp Glu Ala Asn Lys Arg
146     360                 365                 370
148 ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa    1206
149 Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu
150     375                 380                 385
152 gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca    1254
153 Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro
154 390                 395                 400                 405
156 tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca    1302
157 Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr
158                 410                 415                 420
160 tgt act ggc tgt atg caa tat ttc tgt tgg att tgc atg ggt tct ctc    1350
161 Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu
162                 425                 430                 435
164 tct aga gca aac cct tac aaa cat ttc aat gac cct ggt tca cca tgt    1398
165 Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys
166                 440                 445                 450
168 ttt aac cgg ctg ttt tat gct gtg gat gtt gac gac gat att tgg gaa    1446
169 Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp Asp Asp Ile Trp Glu
170     455                 460                 465
172 gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg          1494
173 Asp Glu Val Glu Asp  *
174 470
176 ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt  1554
177 tgcgggatat ttagggtact attcattcac tcttcctgcg tagaagatat ggaagaacga  1614
178 ggtttatatt ttcatgtggt actactgaag aaggtgcatt gatacatttt taaatgtaag  1674
179 ttgagaaaaa tttataagcc aaaggttcag aaaattaaac tacagaa              1721
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 474
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapien
186 <400> SEQUENCE: 2
187 Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
188 1               5                   10                  15
189 Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
190             20                  25                  30
191 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
```

```
192         35                    40                    45
193  Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
194         50                    55                    60
195  Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
196  65                    70                    75                    80
197  Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
198                    85                    90                    95
199  Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
200                   100                   105                   110
201  Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
202                   115                   120                   125
203  Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe
204        130                   135                   140
205  Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln
206  145                   150                   155                   160
207  Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp
208                   165                   170                   175
209  Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu
210                   180                   185                   190
211  Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln
212              195                   200                   205
213  Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe
214        210                   215                   220
215  Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His
216  225                   230                   235                   240
217  Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg
218              245                   250                   255
219  Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser
220              260                   265                   270
221  Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe
222              275                   280                   285
223  Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala
224        290                   295                   300
225  Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln
226  305                   310                   315                   320
227  Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe
228              325                   330                   335
229  Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val
230              340                   345                   350
231  Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp
232        355                   360                   365
233  Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile
234        370                   375                   380
235  Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn
236  385                   390                   395                   400
237  Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly
238              405                   410                   415
239  Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile
240        420                   425                   430
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RAW SEQUENCE LISTING        DATE: 03/31/2006
PATENT APPLICATION: US/10/517,155    TIME: 15:12:17

Input Set : A:\2110800011U6.TXT
Output Set: N:\CRF4\03312006\J517155.raw

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241 Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
242         435                 440                 445
243 Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
244         450                 455                 460
245 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
246 465                 470
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1335
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapien
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)...(1335)
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (750)...(1332)
260 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the
261       C-terminal binding domain
263 <220> FEATURE:
264 <221> NAME/KEY: misc_feature
265 <222> LOCATION: (631)...(783)
266 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
267       cystein rich LIM motif
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (808)...(996)
272 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
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275 <220> FEATURE:
276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: (985)...(1137)
278 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
279       cystein rich LIM motif
281 <220> FEATURE:
282 <221> NAME/KEY: misc_feature
283 <222> LOCATION: (1162)...(1314)
284 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
285       cystein rich LIM motif
287 <400> SEQUENCE: 3
288 atg cca agg tca ggg gct ccc aaa gag cgc cct gcg gag cct ctc acc        48
289 Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
290 1               5                   10                  15
292 cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct       96
293 Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
294             20                  25                  30
296 tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag      144
297 Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
298         35                  40                  45
300 cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct      192
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<210> 11
<211> 32
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT   what about Xaa at location 5?
<222> 2-3, 6-13, 15, 17-18, 20-21, 23-28, 30-31
<223> Xaa can be any amino acid

<400> 11
Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa His
 1                   5                  10                  15
Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
          20          25                  30
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FYI

**RAW SEQUENCE LISTING ERROR SUMMARY**   DATE: 03/31/2006
**PATENT APPLICATION:   US/10/517,155**    TIME: 15:12:18

Input Set : **A:\211080011U6.TXT**
Output Set: **N:\CRF4\03312006\J517155.raw**

<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the**
**Sequence Listing to ensure that a corresponding explanation is presented in the <220>**
**to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:11; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,15,17,18,20,21,23,24,25,26,27
Seq#:11; Xaa Pos. 28,30,31
Seq#:12; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,22,23,25
Seq#:12; Xaa Pos. 26,28,29,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:12; Xaa Pos. 48,49

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
M:341 Repeated in SeqNo=12